



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/733,698

DATE: 10/12/2004

TIME: 12:23:31

Input Set : A:\94-778-H-CO Seq List.ST25.txt

Output Set: N:\CRF4\10122004\J733698.raw

3 <110> APPLICANT: Tryggvason, Karl  
 4 Kallunki, Pekka  
 5 Pyke, Charles  
 7 <120> TITLE OF INVENTION: Laminin Chains: Diagnostic and Therapeutic Use  
 9 <130> FILE REFERENCE: 94-778-H-CO  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/733,698  
 12 <141> CURRENT FILING DATE: 2003-12-11  
 14 <150> PRIOR APPLICATION NUMBER: US 10/227,738  
 15 <151> PRIOR FILING DATE: 2002-08-26  
 17 <150> PRIOR APPLICATION NUMBER: US 09/663,147  
 18 <151> PRIOR FILING DATE: 2000-09-15  
 20 <150> PRIOR APPLICATION NUMBER: US 08/800,593  
 21 <151> PRIOR FILING DATE: 1997-02-18  
 23 <150> PRIOR APPLICATION NUMBER: US 08/317,450  
 24 <151> PRIOR FILING DATE: 1994-10-04  
 26 <160> NUMBER OF SEQ ID NOS: 19  
 28 <170> SOFTWARE: PatentIn version 3.3  
 30 <210> SEQ ID NO: 1  
 31 <211> LENGTH: 20  
 32 <212> TYPE: DNA  
 33 <213> ORGANISM: Artificial sequence  
 35 <220> FEATURE:  
 36 <223> OTHER INFORMATION: Primer  
 38 <400> SEQUENCE: 1  
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 44 <212> TYPE: DNA  
 45 <213> ORGANISM: Artificial sequence  
 47 <220> FEATURE:  
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 54 <210> SEQ ID NO: 3  
 55 <211> LENGTH: 20  
 56 <212> TYPE: DNA  
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 59 <220> FEATURE:  
 60 <223> OTHER INFORMATION: Primer  
 62 <400> SEQUENCE: 3  
 63 cagtaccaga accgagttcg  
 66 <210> SEQ ID NO: 4  
 67 <211> LENGTH: 20

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68 <212> TYPE: DNA
69 <213> ORGANISM: Artificial sequence
71 <220> FEATURE:
72 <223> OTHER INFORMATION: Primer
74 <400> SEQUENCE: 4
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78 <210> SEQ ID NO: 5
79 <211> LENGTH: 20
80 <212> TYPE: DNA
81 <213> ORGANISM: Artificial Sequence
83 <220> FEATURE:
84 <223> OTHER INFORMATION: Primer
86 <400> SEQUENCE: 5
87 ttactgcgga atctcacagc
90 <210> SEQ ID NO: 6
91 <211> LENGTH: 20
92 <212> TYPE: DNA
93 <213> ORGANISM: Artificial Sequence
95 <220> FEATURE:
96 <223> OTHER INFORMATION: Primer
98 <400> SEQUENCE: 6
99 tacactgttc aaccaggggt
102 <210> SEQ ID NO: 7
103 <211> LENGTH: 20
104 <212> TYPE: DNA
105 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <223> OTHER INFORMATION: Primer
110 <400> SEQUENCE: 7
111 aaacaagccc tctcactggt
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115 <211> LENGTH: 20
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117 <213> ORGANISM: Artificial Sequence
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123 gcggagactg tgctgataag
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135 catacctctc tacatggcat
138 <210> SEQ ID NO: 10
139 <211> LENGTH: 20
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141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Primer
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150 <210> SEQ ID NO: 11
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152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
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158 <400> SEQUENCE: 11
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164 <212> TYPE: DNA
165 <213> ORGANISM: Homo sapiens
168 <220> FEATURE:
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170 <222> LOCATION: (118)..(183)
172 <220> FEATURE:
173 <221> NAME/KEY: CDS
174 <222> LOCATION: (118)..(3699)
176 <220> FEATURE:
177 <221> NAME/KEY: polyA_site
178 <222> LOCATION: (4433)..(4433)
180 <220> FEATURE:
181 <221> NAME/KEY: polyA_site
182 <222> LOCATION: (5195)..(5195)
184 <400> SEQUENCE: 12
185 gaccaccta tcgaaggaaa aggaaggcac agcggagcgc agagtgagaa ccaccaaccg
187 aggcgccggg cagcgacccc tgcagcggag acagagactg agcggcccg caccgcc
189 atg cct gcg ctc tgg ctg ggc tgc tgc ctc tgc ttc tcg ctc ctc ctg
190 Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu
191 1 5 10 15
193 ccc gca gcc cgg gcc acc tcc agg agg gaa gtc tgt gat tgc aat ggg
194 Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly
195 20 25 30
197 aag tcc agg cag tgt atc ttt gat cgg gaa ctt cac aga caa act ggt
198 Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
199 35 40 45
201 aat gga ttc cgc tgc ctc aac tgc aat gac aac act gat ggc att cac
202 Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
203 50 55 60
205 tgc gag aag tgc aag aat ggc ttt tac cgg cac aga gaa agg gac cgc
206 Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
207 65 70 75 80
209 tgt ttg ccc tgc aat tgt aac tcc aaa ggt tct ctt agt gct cga tgt
210 Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys

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211      85      90      95
213 gac aac tct gga cgg tgc agc tgt aaa cca ggt gtg aca gga gcc aga      453
214 Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
215      100      105      110
217 tgc gac cga tgt ctg cca ggc ttc cac atg ctc acg gat gcg ggg tgc      501
218 Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
219      115      120      125
221 acc caa gac cag aga ctg cta gac tcc aag tgt gac tgt gac cca gct      549
222 Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
223      130      135      140
225 ggc atc gca ggg ccc tgt gac gcg ggc cgc tgt gtc tgc aag cca gct      597
226 Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala
227 145      150      155      160
229 gtt act gga gaa cgc tgt gat agg tgt cga tca ggt tac tat aat ctg      645
230 Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu
231      165      170      175
233 gat ggg ggg aac cct gag ggc tgt acc cag tgt ttc tgc tat ggg cat      693
234 Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His
235      180      185      190
237 tca gcc agc tgc cgc agc tct gca gaa tac agt gtc cat aag atc acc      741
238 Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr
239      195      200      205
241 tct acc ttt cat caa gat gtt gat ggc tgg aag gct gtc caa cga aat      789
242 Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn
243      210      215      220
245 ggg tct cct gca aag ctc caa tgg tca cag cgc cat caa gat gtg ttt      837
246 Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe
247 225      230      235      240
249 agc tca gcc caa cga cta gat cct gtc tat ttt gtg gct cct gcc aaa      885
250 Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys
251      245      250      255
253 ttt ctt ggg aat caa cag gtg agc tat ggg caa agc ctg tcc ttt gac      933
254 Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp
255      260      265      270
257 tac cgt gtg gac aga gga ggc aga cac cca tct gcc cat gat gtg atc      981
258 Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile
259      275      280      285
261 ctg gaa ggt gct ggt cta cgg atc aca gct ccc ttg atg cca ctt ggc      1029
262 Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly
263      290      295      300
265 aag aca ctg cct tgt ggg ctc acc aag act tac aca ttc agg tta aat      1077
266 Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Phe Arg Leu Asn
267 305      310      315      320
269 gag cat cca agc aat aat tgg agc ccc cag ctg agt tac ttt gag tat      1125
270 Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr
271      325      330      335
273 cga agg tta ctg cgg aat ctc aca gcc ctc cgc atc cga gct aca tat      1173
274 Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr
275      340      345      350

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277	gga gaa tac agt act ggg tac att gac aat gtg acc ctg att tca gcc	1221
278	Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala	
279	355 360 365	
281	cgc cct gtc tct gga gcc cca gca ccc tgg gtt gaa cag tgt ata tgt	1269
282	Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys	
283	370 375 380	
285	cct gtt ggg tac aag ggg caa ttc tgc cag gat tgt gct tct ggc tac	1317
286	Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr	
287	385 390 395 400	
289	aag aga gat tca gcg aga ctg ggg cct ttt ggc acc tgt att cct tgt	1365
290	Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys	
291	405 410 415	
293	aac tgt caa ggg gga ggg gcc tgt gat cca gac aca gga gat tgt tat	1413
294	Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr	
295	420 425 430	
297	tca ggg gat gag aat cct gac att gag tgt gct gac tgc cca att ggt	1461
298	Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly	
299	435 440 445	
301	ttc tac aac gat ccg cac gac ccc cgc agc tgc aag cca tgt ccc tgt	1509
302	Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys	
303	450 455 460	
305	cat aac ggg ttc agc tgc tca gtg att ccg gag acg gag gag gtg gtg	1557
306	His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val	
307	465 470 475 480	
309	tgc aat aac tgc cct ccc ggg gtc acc ggt gcc cgc tgt gag ctc tgt	1605
310	Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys	
311	485 490 495	
313	gct gat ggc tac ttt ggg gac ccc ttt ggt gaa cat ggc cca gtg agg	1653
314	Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg	
315	500 505 510	
317	cct tgt cag ccc tgt caa tgc aac agc aat gtg gac ccc agt gcc tct	1701
318	Pro Cys Gln Pro Cys Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser	
319	515 520 525	
321	ggg aat tgt gac cgg ctg aca ggc agg tgt ttg aag tgt atc cac aac	1749
322	Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn	
323	530 535 540	
325	aca gcc ggc atc tac tgc gac cag tgc aaa gca ggc tac ttc ggg gac	1797
326	Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp	
327	545 550 555 560	
329	cca ttg gct ccc aac cca gca gac aag tgt cga gct tgc aac tgt aac	1845
330	Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn	
331	565 570 575	
333	ccc atg ggc tca gag cct gta gga tgt cga agt gat ggc acc tgt gtt	1893
334	Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val	
335	580 585 590	
337	tgc aag cca gga ttt ggt ggc ccc aac tgt gag cat gga gca ttc agc	1941
338	Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser	
339	595 600 605	
341	tgt cca gct tgc tat aat caa gtg aag att cag atg gat cag ttt atg	1989

VERIFICATION SUMMARY

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Input Set : A:\94-778-H-CO Seq List.ST25.txt

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number